

United States Patent [19]

Gomez et al.

Patent Number: [11]

5,854,280

Date of Patent:

Dec. 29, 1998

[54] ANTIFUNGAL SORDARIDIN DERIVATIVES

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[21] Appl. No.:

669,441

[22] PCT Filed:

Nov. 6, 1995

[86] PCT No.:

PCT/EP95/04331

§ 371 Date:

Oct. 18, 1996

§ 102(e) Date: Oct. 18, 1996

[87] PCT Pub. No.: WO96/14326

PCT Pub. Date: May 17, 1996

Foreign Application Priority Data [30]

Nov. 8, 1994	[EP]	European Pat. Off	94500173
Nov. 8, 1994	[EP]	European Pat. Off	94500175

Int. Cl.⁶ A61K 31/35 U.S. Cl. 514/456; 514/457; 514/460;

549/362; 549/416 Field of Search 549/362, 416;

514/456, 457, 460

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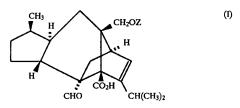
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[57]

ABSTRACT

A compound of formula



wherein Z is a tetrahydro-pyrano group selected from

$$\begin{array}{c} R^2 \quad R^3 \\ X \cdot \cdots \cdot (CR^5R^6)n \\ \vdots \\ Y \\ O \quad R^4 \end{array}$$

$$\bigvee_{O}^{R_{R^{15}}^{15}}$$
 (b)

having antifungal activity processes for their preparation and their use in medicines.

15 Claims, No Drawings

10/21/2002, EAST Version: 1.03.0002

US-PAT-NO: 5854280

DOCUMENT-IDENTIFIER: US 5854280 A

TITLE: Antifungal sordaridin derivatives

----- KWIC -----

NCIMB 40675 is an aerobic, Gram-positive, non-motile irregular rod that

produces lemon yellow, translucent, round, entire, convex colonies with a

diameter of between 0.5-1 mm when grown on tryptic soy agar supplemented with

2% (w/v) yeast extract for 48 hours at 28.degree. C. The organism grows well

at temperatures up to 37.degree. C., but not at 45.degree.

C. Metachromatic

granules were not observed and the strain is catalase positive, oxidase

negative and does not metabolise glucose fermentatively. The strain can

utilise the following sources of carbon: .alpha.-D-glucose, D-fructose,

p-hydroxyphenyl-acetic acid, D-mannitol, methylpyruvate, lactamide, D-trehalose

and sucrose. The organism can only weakly utilise D-gluconic acid, pyruvic

acid and salicin as sole carbon sources. Colony and microscopic morphology

resembles that of coryneform bacteria. The genus Corynebacterium was excluded

on the grounds that the peptidoglycan of NCIMB 40675 contains omithine rather

than the meso-isomer of 2,6-diaminopimelic acid or diaminobutyric acid. Also,

the organism contains a complex mixture of branch chain fatty acids atypical of

Corynebacterium species, namely, 12-methyltetradecanoic, 14-methylhexadecanoic

and 14-methylpentadecanoic acids. The presence of .alpha.-branched-.beta.-hydroxylated fatty acids was not determined. On the

basis of these results NCIMB 40675 most closely resembles

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one of the following actinobacterial genera: Aureobacterium, Curtobacterium or Cellulomonas.

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